

3060 DC



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DATE: 02/11/2003

PATENT APPLICATION: US/10/031,722

TIME: 13:44:28

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3 <110> APPLICANT: Keler, Tibor
 4 Deo, Yashwant
 6 <120> TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HER2/NEU
 8 <130> FILE REFERENCE: MXI-160US
 10 <140> CURRENT APPLICATION NUMBER: US 10/031,722
 C--> 11 <141> CURRENT FILING DATE: 2002-10-15
 13 <150> PRIOR APPLICATION NUMBER: PCT/US00/20272
 14 <151> PRIOR FILING DATE: 2000-07-25
 16 <150> PRIOR APPLICATION NUMBER: US 60/146,313
 17 <151> PRIOR FILING DATE: 1999-07-29
 19 <150> PRIOR APPLICATION NUMBER: US 60/188,539
 20 <151> PRIOR FILING DATE: 1999-03-10
 22 <160> NUMBER OF SEQ ID NOS: 13
 24 <170> SOFTWARE: PatentIn Ver. 2.0
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 27 <211> LENGTH: 372
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 33 <222> LOCATION: (1)..(372)
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 38 1 5 10 15
 40 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agc agc tat 96
 41 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 42 20 25 30
 44 gcc atg acc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc 144
 45 Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 46 35 40 45
 48 tca gct atc agt ggt agt ggt tat agc aca tac tac gca gac tcc gag 192
 49 Ser Ala Ile Ser Gly Ser Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Glu
 50 50 55 60
 52 aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240
 53 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 54 65 70 75 80
 56 ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta tat tac tgt 288
 57 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 58 85 90 95
 60 gcg aaa ggg ttt cag tat ggt tcg ggg agt tat tat acc cac ttt gac 336
 61 Ala Lys Gly Phe Gln Tyr Gly Ser Gly Ser Tyr Tyr Thr His Phe Asp
 62 100 105 110

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82 Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
83      35      40      45
85 Ser Ala Ile Ser Gly Ser Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Glu
86      50      55      60
88 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
89  65      70      75      80
91 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
92      85      90      95
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121      35      40      45
123 tat gct gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agc ggc 192
124 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
125      50      55      60
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128 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
129  65      70      75      80
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150 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
151          20          25          30
153 Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
154          35          40          45
156 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
157          50          55          60
159 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
160 65          70          75          80
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184 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
185          20          25          30
187 gac ata cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
188 Asp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
189          35          40          45
191 gca gta ata tgg tat gat ggc agt aat aaa tac cat gca gac tcc gtg 192
192 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr His Ala Asp Ser Val
193          50          55          60
195 aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240
196 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
197 65          70          75          80
199 ctg caa atg aac agt ctg aga gcc gag gac acg gct gtg tat tac tgt 288
200 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
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223          20          25          30
225 Asp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
226          35          40          45
228 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr His Ala Asp Ser Val
229          50          55          60
231 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
232 65          70          75          80
234 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
235          85          90          95
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256 1          5          10          15
258 gac aga gtc acc atc act tgt cgg gcg agt cat ggt att agc agc tgg 96
259 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Gly Ile Ser Ser Trp
260          20          25          30
262 tta gcc tgg tat cag cag aaa cca gag aaa gcc cct aag tcc ctg atc 144
263 Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
264          35          40          45
266 tat gct gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agc ggc 192
267 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
268          50          55          60
270 agt gga tct ggg aca gat ttc act ctc acc atc agc agc ctg cag cct 240
271 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

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272 65          70          75          80
274 gaa gat ttt gca act tat tac tgc caa cag tat aat agt tac ccg tac 288
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280          100          105
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286 <212> TYPE: PRT
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296 Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
297 35 40 45
299 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
300 50 55 60
302 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
303 65 70 75 80
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308 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
309 100 105
312 <210> SEQ ID NO: 9
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314 <212> TYPE: DNA
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317 <220> FEATURE:
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324 1 5 10 15
326 tcc ctg aga ctc tcc tgt gca gcg tct gga ttc acc ttc agt agc tat 96
327 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
328 20 25 30
330 gtc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
331 Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
332 35 40 45
334 gca gtt ata tgg tat gat gga agt aat aaa tac tat gca gac tcc gtg 192
335 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
336 50 55 60
338 aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240
339 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
340 65 70 75 80

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VERIFICATION SUMMARY

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